

[illegible]

tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg 300  
 Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val  
 65 70 75

cat	caa	gta	gaa	gaa	tgc	agg	gtt	aaa	ggg	cct	gga	atc	tca	aaa	ttt	348
His	Gln	Val	Glu	Glu	Cys	Arg	Val	Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	
	80					85					90					
gtt	cag	aaa	gta	aat	gaa	ata	ggc	att	tac	ctg	act	gat	tgc	atg	gaa	396
Val	Gln	Lys	Val	Asn	Glu	Ile	Gly	Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	
95				100						105					110	
aga	gct	agg	gaa	gtg	att	cca	agg	tcc	cag	cac	caa	gag	aca	ccc	gtt	444
Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg	Ser	Gln	His	Gln	Glu	Thr	Pro	Val	
			115						120					125		
tac	ctg	gga	gcc	acg	gca	ggc	atg	cgg	ttg	ctc	agg	atg	gaa	agt	gaa	492
Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met	Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	
			130					135					140			
gag	ttg	gca	gac	agg	gtt	ctg	gat	gtg	gtg	gag	agg	agc	ctc	agc	aac	540
Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp	Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	
		145					150					155				
tac	ccc	ttt	gac	ttc	cag	ggg	gcc	agg	atc	att	act	ggc	caa	gag	gaa	588
Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala	Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	
	160					165					170					
ggg	gcc	tat	ggc	tgg	att	act	atc	aac	tat	ctg	ctg	ggc	aaa	ttc	agt	636
Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile	Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	
175					180					185					190	
cag	aaa	aca	agg	tgg	ttc	agc	ata	gtc	cca	tat	gaa	acc	aat	aat	cag	684
Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile	Val	Pro	Tyr	Glu	Thr	Asn	Asn	Gln	
				195					200					205		
gaa	acc	ttt	gga	gct	ttg	gac	ctt	ggg	gga	gcc	tct	aca	caa	gtc	act	732
Glu	Thr	Phe	Gly	Ala	Leu	Asp	Leu	Gly	Gly	Ala	Ser	Thr	Gln	Val	Thr	
			210					215					220			
ttt	gta	ccc	caa	aac	cag	act	atc	gag	tcc	cca	gat	aat	gct	ctg	caa	780
Phe	Val	Pro	Gln	Asn	Gln	Thr	Ile	Glu	Ser	Pro	Asp	Asn	Ala	Leu	Gln	
		225					230					235				
ttt	cgc	ctc	tat	ggc	aag	gac	tac	aat	gtc	tac	aca	cat	agc	ttc	ttg	828
Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu	
	240					245					250					
tgc	tat	ggg	aag	gat	cag	gca	ctc	tgg	cag	aaa	ctg	gcc	aag	gac	att	876
Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile	
255					260					265					270	
cag	gtt	gca	agt	aat	gaa	att	ctc	agg	gac	cca	tgc	ttt	cat	cct	gga	924
Gln	Val	Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly	
				275					280					285		
tat	aag	aag	gta	gtg	aac	gta	agt	gac	ctt	tac	aag	acc	ccc	tgc	acc	972
Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr	
			290					295					300			
aag	aga	ttt	gag	atg	act	ctt	cca	ttc	cag	cag	ttt	gaa	atc	cag	ggg	1020
Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	
		305					310					315				

att gga aac tat caa caa tgc cat caa agc atc ctg gag ctc ttc aac	1068
Ile Gly Asn Tyr Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn	
320 325 330	
acc agt tac tgc cct tac tcc cag tgt gcc ttc aat ggg att ttc ttg	1116
Thr Ser Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu	
335 340 345 350	
cca cca ctc cag ggg gat ttt ggg gca ttt tca gct ttt tac ttt gtg	1164
Pro Pro Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val	
355 360 365	
atg aag ttt tta aac ttg aca tca gag aaa gtc tct cag gaa aag gtg	1212
Met Lys Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val	
370 375 380	
act gag atg atg aaa aag ttc tgt gct cag cct tgg gag gag ata aaa	1260
Thr Glu Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys	
385 390 395	
aca tct tac gct gga gta aag gag aag tac ctg agt gaa tac tgc ttt	1308
Thr Ser Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe	
400 405 410	
tct ggt acc tac att ctc tcc ctc ctt ctg caa ggc tat cat ttc aca	1356
Ser Gly Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr	
415 420 425 430	
gct gat tcc tgg gag cac atc cat ttc att ggc aag atc cag ggc agc	1404
Ala Asp Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser	
435 440 445	
gac gcc ggc tgg act ttg ggc tac atg ctg aac ctg acc aac atg atc	1452
Asp Ala Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile	
450 455 460	
cca gct gag caa cca ttg tcc aca cct ctc tcc cac tcc acc tat gtc	1500
Pro Ala Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val	
465 470 475	
ttc ctc atg gtt cta ttc tcc ctg gtc ctt ttc aca gtg gcc atc ata	1548
Phe Leu Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile	
480 485 490	
ggc ttg ctt atc ttt cac aag cct tca tat ttc tgg aaa gat atg gta	1596
Gly Leu Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val	
495 500 505 510	
tag	1599

<210> 2  
 <211> 510  
 <212> PRT  
 <213> Homo sapiens

<400> 2  
 Met Glu Asp Thr Lys Glu Ser Asn Val Lys Thr Phe Cys Ser Lys Asn  
 1 5 10 15



Tyr Cys Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro  
 340 345 350  
 Leu Gln Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys  
 355 360 365  
 Phe Leu Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu  
 370 375 380  
 Met Met Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser  
 385 390 395 400  
 Tyr Ala Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly  
 405 410 415  
 Thr Tyr Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp  
 420 425 430  
 Ser Trp Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala  
 435 440 445  
 Gly Trp Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala  
 450 455 460  
 Glu Gln Pro Leu Ser Thr Pro Leu Ser His Ser Thr Tyr Val Phe Leu  
 465 470 475 480  
 Met Val Leu Phe Ser Leu Val Leu Phe Thr Val Ala Ile Ile Gly Leu  
 485 490 495  
 Leu Ile Phe His Lys Pro Ser Tyr Phe Trp Lys Asp Met Val  
 500 505 510

<210> 3

<211> 476

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 3

Met Ala Thr Ser Trp Gly Thr Val Phe Phe Met Leu Val Val Ser Cys  
 1 5 10 15  
 Val Cys Ser Ala Val Ser His Arg Asn Gln Gln Thr Trp Phe Glu Gly  
 20 25 30  
 Ile Phe Leu Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys  
 35 40 45  
 Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile  
 50 55 60  
 Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln  
 65 70 75 80  
 Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln









SECRET

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<220>
<221> CDS
<222> (1) .. (1362)
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1				5					10					15			
cag	aac	aaa	gca	ttg	cca	gaa	aac	gtt	aag	tat	ggg	att	gtg	ctg	gat		96
Gln	Asn	Lys	Ala	Leu	Pro	Glu	Asn	Val	Lys	Tyr	Gly	Ile	Val	Leu	Asp		
			20					25					30				
gcg	ggt	tct	tct	cac	aca	agt	tta	tac	atc	tat	aag	tgg	cca	gca	gaa		144
Ala	Gly	Ser	Ser	His	Thr	Ser	Leu	Tyr	Ile	Tyr	Lys	Trp	Pro	Ala	Glu		
		35					40					45					
aag	gag	aat	gac	aca	ggc	gtg	gtg	cat	caa	gta	gaa	gaa	tgc	agg	gtt		192
Lys	Glu	Asn	Asp	Thr	Gly	Val	Val	His	Gln	Val	Glu	Glu	Cys	Arg	Val		
	50					55					60						
aaa	ggt	cct	gga	atc	tca	aaa	ttt	gtt	cag	aaa	gta	aat	gaa	ata	ggc		240
Lys	Gly	Pro	Gly	Ile	Ser	Lys	Phe	Val	Gln	Lys	Val	Asn	Glu	Ile	Gly		
65					70					75				80			
att	tac	ctg	act	gat	tgc	atg	gaa	aga	gct	agg	gaa	gtg	att	cca	agg		288
Ile	Tyr	Leu	Thr	Asp	Cys	Met	Glu	Arg	Ala	Arg	Glu	Val	Ile	Pro	Arg		
				85					90					95			
tcc	cag	cac	caA	gag	aca	ccc	gtt	tac	ctg	gga	gcc	acg	gca	ggc	atg		336
Ser	Gln	His	Gln	Glu	Thr	Pro	Val	Tyr	Leu	Gly	Ala	Thr	Ala	Gly	Met		
			100					105					110				
cgg	ttg	ctc	agg	atg	gaa	agt	gaa	gag	ttg	gca	gac	agg	gtt	ctg	gat		384
Arg	Leu	Leu	Arg	Met	Glu	Ser	Glu	Glu	Leu	Ala	Asp	Arg	Val	Leu	Asp		
		115					120					125					
gtg	gtg	gag	agg	agc	ctc	agc	aac	tac	ccc	ttt	gac	ttc	cag	ggt	gcc		432
Val	Val	Glu	Arg	Ser	Leu	Ser	Asn	Tyr	Pro	Phe	Asp	Phe	Gln	Gly	Ala		
	130					135					140						
agg	atc	att	act	ggc	caa	gag	gaa	ggt	gcc	tat	ggc	tgg	att	act	atc		480
Arg	Ile	Ile	Thr	Gly	Gln	Glu	Glu	Gly	Ala	Tyr	Gly	Trp	Ile	Thr	Ile		
145					150				155						160		
aac	tat	ctg	ctg	ggc	aaa	ttc	agt	cag	aaa	aca	agg	tgg	ttc	agc	ata		528
Asn	Tyr	Leu	Leu	Gly	Lys	Phe	Ser	Gln	Lys	Thr	Arg	Trp	Phe	Ser	Ile		
				165					170					175			
gtc	cca	tat	gaa	acc	aat	aat	cag	gaa	acc	ttt	gga	gct	ttg	gac	ctt		576

Val	Pro	Tyr	Glu 180	Thr	Asn	Asn	Gln	Glu 185	Thr	Phe	Gly	Ala	Leu 190	Asp	Leu	
ggg Gly	gga Gly	gcc Ala 195	tct Ser	aca Thr	caa Gln	gtc Val	act Thr 200	ttt Phe	gta Val	ccc Pro	caa Gln	aac Asn 205	cag Gln	act Thr	atc Ile	624
gag Glu	tcc Ser 210	cca Pro	gat Asp	aat Asn	gct Ala	ctg Leu 215	caa Gln	ttt Phe	cgc Arg	ctc Leu	tat Tyr 220	ggc Gly	aag Lys	gac Asp	tac Tyr	672
aat Asn 225	gtc Val	tac Tyr	aca Thr	cat His	agc Ser 230	ttc Phe	ttg Leu	tgc Cys	tat Tyr	ggg Gly 235	aag Lys	gat Asp	cag Gln	gca Ala	ctc Leu 240	720
tgg Trp	cag Gln	aaa Lys	ctg Leu	gcc Ala 245	aag Lys	gac Asp	att Ile	cag Gln	gtt Val 250	gca Ala	agt Ser	aat Asn	gaa Glu	att Ile 255	ctc Leu	768
agg Arg	gac Asp	cca Pro	tgc Cys 260	ttt Phe	cat His	cct Pro	gga Gly	tat Tyr 265	aag Lys	aag Lys	gta Val	gtg Val	aac Asn 270	gta Val	agt Ser	816
gac Asp	ctt Leu	tac Tyr 275	aag Lys	acc Thr	ccc Pro	tgc Cys	acc Thr 280	aag Lys	aga Arg	ttt Phe	gag Glu	atg Met 285	act Thr	ctt Leu	cca Pro	864
ttc Phe	cag Gln 290	cag Gln	ttt Phe	gaa Glu	atc Ile	cag Gln 295	ggg Gly	att Ile	gga Gly	aac Asn	tat Tyr 300	caa Gln	caa Gln	tgc Cys	cat His	912
caa Gln 305	agc Ser	atc Ile	ctg Leu	gag Glu	ctc Leu 310	ttc Phe	aac Asn	acc Thr	agt Ser	tac Tyr 315	tgc Cys	cct Pro	tac Tyr	tcc Ser	cag Gln 320	960
tgt Cys	gcc Ala	ttc Phe	aat Asn	ggg Gly 325	att Ile	ttc Phe	ttg Leu	cca Pro	cca Pro 330	ctc Leu	cag Gln	ggg Gly	gat Asp	ttt Phe 335	ggg Gly	1008
gca Ala	ttt Phe	tca Ser	gct Ala 340	ttt Phe	tac Tyr	ttt Phe	gtg Val 345	atg Met	aag Lys	ttt Phe	tta Leu	aac Asn 350	ttg Leu	aca Thr	tca Ser	1056
gag Glu	aaa Lys	gtc Val 355	tct Ser	cag Gln	gaa Glu	aag Lys	gtg Val 360	act Thr	gag Glu	atg Met	atg Met	aaa Lys 365	aag Lys	ttc Phe	tgt Cys	1104
gct Ala	cag Gln 370	cct Pro	tgg Trp	gag Glu	gag Glu	ata Ile 375	aaa Lys	aca Thr	tct Ser	tac Tyr	gct Ala 380	gga Gly	gta Val	aag Lys	gag Glu	1152
aag Lys 385	tac Tyr	ctg Leu	agt Ser	gaa Glu	tac Tyr 390	tgc Cys	ttt Phe	tct Ser	ggg Gly	acc Thr 395	tac Tyr	att Ile	ctc Leu	tcc Ser	ctc Leu 400	1200
ctt Leu	ctg Leu	caa Gln	ggc Gly	tat Tyr 405	cat His	ttc Phe	aca Thr	gct Ala	gat Asp 410	tcc Ser	tgg Trp	gag Glu	cac His	atc Ile 415	cat His	1248
ttc	att	ggc	aag	atc	cag	ggc	agc	gac	gcc	ggc	tgg	act	ttg	ggc	tac	1296





<221> CDS

<222> (1)..(1434)

<400> 7

atg gcc ctg tgg atc gac agg atg caa ctc ctg tct tgc att gca cta	48
Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu	
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agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag	96
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys	
20 25 30	
aaa aca cag cta act agt tca acc cag aac aaa gca ttg cca gaa aac	144
Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn	
35 40 45	
gtt aag tat ggg att gtg ctg gat gcg ggt tct tct cac aca agt tta	192
Val Lys Tyr Gly Ile Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu	
50 55 60	
tac atc tat aag tgg cca gca gaa aag gag aat gac aca ggc gtg gtg	240
Tyr Ile Tyr Lys Trp Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val	
65 70 75 80	
cat caa gta gaa gaa tgc agg gtt aaa ggt cct gga atc tca aaa ttt	288
His Gln Val Glu Glu Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe	
85 90 95	
gtt cag aaa gta aat gaa ata ggc att tac ctg act gat tgc atg gaa	336
Val Gln Lys Val Asn Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu	
100 105 110	
aga gct agg gaa gtg att cca agg tcc cag cac caa gag aca ccc gtt	384
Arg Ala Arg Glu Val Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val	
115 120 125	
tac ctg gga gcc acg gca ggc atg cgg ttg ctc agg atg gaa agt gaa	432
Tyr Leu Gly Ala Thr Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu	
130 135 140	
gag ttg gca gac agg gtt ctg gat gtg gtg gag agg agc ctc agc aac	480
Glu Leu Ala Asp Arg Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn	
145 150 155 160	
tac ccc ttt gac ttc cag ggt gcc agg atc att act ggc caa gag gaa	528
Tyr Pro Phe Asp Phe Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu	
165 170 175	
ggg gcc tat ggc tgg att act atc aac tat ctg ctg ggc aaa ttc agt	576
Gly Ala Tyr Gly Trp Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser	
180 185 190	
cag aaa aca agg tgg ttc agc ata gtc cca tat gaa acc aat aat cag	624
Gln Lys Thr Arg Trp Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln	
195 200 205	
gaa acc ttt gga gct ttg gac ctt ggg gga gcc tct aca caa gtc act	672
Glu Thr Phe Gly Ala Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr	
210 215 220	

ttt Phe 225	gta Val	ccc Pro	caa Gln	aac Asn	cag Gln 230	act Thr	atc Ile	gag Glu	tcc Ser	cca Pro 235	gat Asp	aat Asn	gct Ala	ctg Leu	caa Gln 240	720
ttt Phe	cgc Arg	ctc Leu	tat Tyr	ggc Gly 245	aag Lys	gac Asp	tac Tyr	aat Asn	gtc Val 250	tac Tyr	aca Thr	cat His	agc Ser	ttc Phe 255	ttg Leu	768
tgc Cys	tat Tyr	ggg Gly	aag Lys 260	gat Asp	cag Gln	gca Ala	ctc Leu	tgg Trp 265	cag Gln	aaa Lys	ctg Leu	gcc Ala	aag Lys 270	gac Asp	att Ile	816
cag Gln	gtt Val	gca Ala 275	agt Ser	aat Asn	gaa Glu	att Ile	ctc Leu 280	agg Arg	gac Asp	cca Pro	tgc Cys	ttt Phe 285	cat His	cct Pro	gga Gly	864
tat Tyr	aag Lys 290	aag Lys	gta Val	gtg Val	aac Asn	gta Val 295	agt Ser	gac Asp	ctt Leu	tac Tyr	aag Lys 300	acc Thr	ccc Pro	tgc Cys	acc Thr	912
aag Lys 305	aga Arg	ttt Phe	gag Glu	atg Met	act Thr 310	ctt Leu	cca Pro	ttc Phe	cag Gln	cag Gln 315	ttt Phe	gaa Glu	atc Ile	cag Gln	ggc Gly 320	960
att Ile	gga Gly	aac Asn	tat Tyr	caa Gln 325	caa Gln	tgc Cys	cat His	caa Gln	agc Ser 330	atc Ile	ctg Leu	gag Glu	ctc Leu	ttc Phe 335	aac Asn	1008
acc Thr	agt Ser	tac Tyr	tgc Cys 340	cct Pro	tac Tyr	tcc Ser	cag Gln	tgt Cys 345	gcc Ala	ttc Phe	aat Asn	ggg Gly	att Ile 350	ttc Phe	ttg Leu	1056
cca Pro	cca Pro	ctc Leu 355	cag Gln	ggg Gly	gat Asp	ttt Phe	ggg Gly 360	gca Ala	ttt Phe	tca Ser	gct Ala	ttt Phe 365	tac Tyr	ttt Phe	gtg Val	1104
atg Met	aag Lys 370	ttt Phe	tta Leu	aac Asn	ttg Leu	aca Thr 375	tca Ser	gag Glu	aaa Lys	gtc Val	tct Ser	cag Gln	gaa Glu	aag Lys	gtg Val	1152
act Thr 385	gag Glu	atg Met	atg Met	aaa Lys	aag Lys 390	ttc Phe	tgt Cys	gct Ala	cag Gln	cct Pro 395	tgg Trp	gag Glu	gag Glu	ata Ile	aaa Lys 400	1200
aca Thr	tct Ser	tac Tyr	gct Ala 405	gga Gly	gta Val	aag Lys	gag Glu	aag Lys	tac Tyr 410	ctg Leu	agt Ser	gaa Glu	tac Tyr	tgc Cys 415	ttt Phe	1248
tct Ser	ggc Gly	acc Thr	tac Tyr 420	att Ile	ctc Leu	tcc Ser	ctc Leu	ctt Leu 425	ctg Leu	caa Gln	ggc Gly	tat Tyr	cat His 430	ttc Phe	aca Thr	1296
gct Ala	gat Asp	tcc Ser 435	tgg Trp	gag Glu	cac His	atc Ile	cat His 440	ttc Phe	att Ile	ggc Gly	aag Lys	atc Ile 445	cag Gln	ggc Gly	agc Ser	1344
gac Asp	gcc Ala 450	ggc Gly	tgg Trp	act Thr	ttg Leu	ggc Gly 455	tac Tyr	atg Met	ctg Leu	aac Asn	ctg Leu 460	acc Thr	aac Asn	atg Met	atc Ile	1392



Phe	Arg	Leu	Tyr	Gly	Lys	Asp	Tyr	Asn	Val	Tyr	Thr	His	Ser	Phe	Leu
				245					250					255	
Cys	Tyr	Gly	Lys	Asp	Gln	Ala	Leu	Trp	Gln	Lys	Leu	Ala	Lys	Asp	Ile
			260					265					270		
Gln	Val	Ala	Ser	Asn	Glu	Ile	Leu	Arg	Asp	Pro	Cys	Phe	His	Pro	Gly
		275					280					285			
Tyr	Lys	Lys	Val	Val	Asn	Val	Ser	Asp	Leu	Tyr	Lys	Thr	Pro	Cys	Thr
	290					295					300				
Lys	Arg	Phe	Glu	Met	Thr	Leu	Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly
305					310					315					320
Ile	Gly	Asn	Tyr	Gln	Gln	Cys	His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn
				325					330					335	
Thr	Ser	Tyr	Cys	Pro	Tyr	Ser	Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu
			340					345					350		
Pro	Pro	Leu	Gln	Gly	Asp	Phe	Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val
		355					360					365			
Met	Lys	Phe	Leu	Asn	Leu	Thr	Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val
	370					375					380				
Thr	Glu	Met	Met	Lys	Lys	Phe	Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys
385					390					395					400
Thr	Ser	Tyr	Ala	Gly	Val	Lys	Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe
				405					410					415	
Ser	Gly	Thr	Tyr	Ile	Leu	Ser	Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr
			420					425					430		
Ala	Asp	Ser	Trp	Glu	His	Ile	His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser
		435					440					445			
Asp	Ala	Gly	Trp	Thr	Leu	Gly	Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile
	450					455					460				
Pro	Ala	Glu	Gln	Pro	Leu	Ser	Thr	Pro	Leu	Ser	His	Ser	Thr		
465					470					475					

<210> 9

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
signal sequence

<400> 9

Met	Ala	Leu	Trp	Ile	Asp	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu
1					5				10					15	

Ser Leu Ala Leu Val Thr Asn Ser



<210> 10  
 <211> 8  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Synthetic peptide

<400> 10  
 Asp Tyr Lys Asp Asp Asp Asp Lys  
     1                    5

<210> 11  
 <211> 43  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 11  
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
     1                    5                    10                    15

Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
                     20                    25                    30

Lys Thr Gln Leu Thr Ser Ser Thr Gln Asn Lys  
             35                    40

<210> 12  
 <211> 29  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence: Fusion construct of human CD39

<400> 12  
 Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
     1                    5                    10                    15

Ser Leu Ala Leu Val Thr Asn Ser Ala Thr Gln Asn Lys  
                     20                    25

<210> 13  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 13

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ala Ser Ser Thr Gln Asn Lys  
20 25 30

<210> 14

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 14

cgggctggac ttggtggtac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60

tgtccacacc tctctcccac gagcccc 87

<210> 15

<211> 87

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 15

gatcggggct cgtgggagag aggtgtggac aatgggtgct cagctgggat catgttggtc 60

aggttcagca tgtagcccaa agtccag 87

<210> 16

<211> 740

<212> DNA

<213> Homo sapiens

<220>

<221> CDS

<222> (42)..(737)

<400> 16

cgtaccgct agcgtcgaca ggcctaggat atcgatacgt a gag ccc aga tct tgt 56  
Glu Pro Arg Ser Cys  
1 5

gac aaa act cac aca tgc cca ccg tgc cca gca cct gaa gcc gag ggc 104  
Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu Ala Glu Gly  
10 15 20

[illegible]

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<210> 17
<211> 232
<212> PRT
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[illegible]

Glu Pro Arg Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala  
1 5 10 15

Lys Asp Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val  
35 40 45

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln  
65 70 75 80

Asp Trp Leu Asn Gly Lys Asp Tyr Lys Cys Lys Val Ser Asn Lys Ala  
100 105 110

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Asp Glu Leu Thr  
130 135 140

His Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr  
165 170 175

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe  
195 200 205

Ser Leu Ser Leu Ser Pro Gly Lys  
225 230

<400> 18

ctttccatcc tgagcaac

18

<210> 19

<211> 36

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 19

aaaaaactag tcagaacaaa gctttgccag aaaacg

36

<210> 20

<211> 24

<212> PRT

<213> Mus sp.

<400> 20

Met Phe His Val Ser Phe Arg Tyr Ile Phe Gly Ile Pro Pro Leu Ile  
1 5 10 15

Leu Val Leu Leu Pro Val Thr Ser  
20

<210> 21

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 21

ctagttctgg agactacaaa gatgacgatg acaaaaccga gaacaa

46

<210> 22

<211> 46

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 22

agctttgttc tgggttttgc catcgatc tttgtagtct ccagaa

46

<210> 23

<211> 89

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 23

ccggctggac tttgggctac atgctgaacc tgaccaacat gatcccagct gagcaaccat 60  
tgtccacacc tctctccac tccacctaa 89

<210> 24

<211> 89

<212> DNA

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Synthetic  
oligonucleotide

<400> 24

ggccttaggt ggagtgggag agaggtgtgg acaatggtg ctcagctggg atcatgttgg 60  
tcaggttcag catgtagccc aaagtccag 89

<210> 25

<211> 1464

<212> DNA

<213> Artificial Sequence

<220>

<221> CDS

<222> (1)..(1461)

<220>

<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 25

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Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15  
agt ctt gca ctt gtc aca aac agt gca cct act tca agt tct aca aag 96  
Ser Leu Ala Leu Val Thr Asn Ser Ala Pro Thr Ser Ser Ser Thr Lys  
20 25 30  
aaa aca cag cta act agt tca gga gac tac aaa gat gac gat gac aaa 144  
Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys  
35 40 45  
acc cag aac aaa gca ttg cca gaa aac gtt aag tat ggg att gtg ctg 192  
Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu  
50 55 60  
gat gcg ggt tct tct cac aca agt tta tac atc tat aag tgg cca gca 240  
Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala  
65 70 75 80  
gaa aag gag aat gac aca ggc gtg gtg cat caa gta gaa gaa tgc agg 288



Pro	Phe	Gln	Gln	Phe	Glu	Ile	Gln	Gly	Ile	Gly	Asn	Tyr	Gln	Gln	Cys		
				325					330					335			
cat	caa	agc	atc	ctg	gag	ctc	ttc	aac	acc	agt	tac	tgc	cct	tac	tcc	1056	
His	Gln	Ser	Ile	Leu	Glu	Leu	Phe	Asn	Thr	Ser	Tyr	Cys	Pro	Tyr	Ser		
			340					345					350				
cag	tgt	gcc	ttc	aat	ggg	att	ttc	ttg	cca	cca	ctc	cag	ggg	gat	ttt	1104	
Gln	Cys	Ala	Phe	Asn	Gly	Ile	Phe	Leu	Pro	Pro	Leu	Gln	Gly	Asp	Phe		
		355					360					365					
ggg	gca	ttt	tca	gct	ttt	tac	ttt	gtg	atg	aag	ttt	tta	aac	ttg	aca	1152	
Gly	Ala	Phe	Ser	Ala	Phe	Tyr	Phe	Val	Met	Lys	Phe	Leu	Asn	Leu	Thr		
	370					375					380						
tca	gag	aaa	gtc	tct	cag	gaa	aag	gtg	act	gag	atg	atg	aaa	aag	ttc	1200	
Ser	Glu	Lys	Val	Ser	Gln	Glu	Lys	Val	Thr	Glu	Met	Met	Lys	Lys	Phe		
385					390				395						400		
tgt	gct	cag	cct	tgg	gag	gag	ata	aaa	aca	tct	tac	gct	gga	gta	aag	1248	
Cys	Ala	Gln	Pro	Trp	Glu	Glu	Ile	Lys	Thr	Ser	Tyr	Ala	Gly	Val	Lys		
				405					410					415			
gag	aag	tac	ctg	agt	gaa	tac	tgc	ttt	tct	ggt	acc	tac	att	ctc	tcc	1296	
Glu	Lys	Tyr	Leu	Ser	Glu	Tyr	Cys	Phe	Ser	Gly	Thr	Tyr	Ile	Leu	Ser		
			420					425					430				
ctc	ctt	ctg	caa	ggc	tat	cat	ttc	aca	gct	gat	tcc	tgg	gag	cac	atc	1344	
Leu	Leu	Leu	Gln	Gly	Tyr	His	Phe	Thr	Ala	Asp	Ser	Trp	Glu	His	Ile		
			435				440					445					
cat	ttc	att	ggc	aag	atc	cag	ggc	agc	gac	gcc	ggc	tgg	act	ttg	ggc	1392	
His	Phe	Ile	Gly	Lys	Ile	Gln	Gly	Ser	Asp	Ala	Gly	Trp	Thr	Leu	Gly		
	450					455				460							
tac	atg	ctg	aac	ctg	acc	aac	atg	atc	cca	gct	gag	caa	cca	ttg	tcc	1440	
Tyr	Met	Leu	Asn	Leu	Thr	Asn	Met	Ile	Pro	Ala	Glu	Gln	Pro	Leu	Ser		
465					470				475						480		
aca	cct	ctc	tcc	cac	tcc	acc	taa									1464	
Thr	Pro	Leu	Ser	His	Ser	Thr											
				485													

<210> 26

<211> 487

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 26

Met	Ala	Leu	Trp	Ile	Asp	Arg	Met	Gln	Leu	Leu	Ser	Cys	Ile	Ala	Leu
1				5				10					15		
Ser	Leu	Ala	Leu	Val	Thr	Asn	Ser	Ala	Pro	Thr	Ser	Ser	Ser	Thr	Lys
			20					25				30			



Lys Thr Gln Leu Thr Ser Ser Gly Asp Tyr Lys Asp Asp Asp Asp Lys  
 35 40 45  
 Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile Val Leu  
 50 55 60  
 Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp Pro Ala  
 65 70 75 80  
 Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu Cys Arg  
 85 90 95  
 Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn Glu Ile  
 100 105 110  
 Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val Ile Pro  
 115 120 125  
 Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr Ala Gly  
 130 135 140  
 Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg Val Leu  
 145 150 155 160  
 Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe Gln Gly  
 165 170 175  
 Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp Ile Thr  
 180 185 190  
 Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp Phe Ser  
 195 200 205  
 Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala Leu Asp  
 210 215 220  
 Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn Gln Thr  
 225 230 235 240  
 Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly Lys Asp  
 245 250 255  
 Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp Gln Ala  
 260 265 270  
 Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn Glu Ile  
 275 280 285  
 Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val Asn Val  
 290 295 300  
 Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met Thr Leu  
 305 310 315 320  
 Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln Gln Cys  
 325 330 335  
 His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys Pro Tyr Ser  
 340 345 350

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210	215	220
Asn Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr 225 230 235 240		
Gly Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys 245 250 255		
Asp Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser 260 265 270		
Asn Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val 275 280 285		
Val Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu 290 295 300		
Met Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr 305 310 315 320		
Gln Gln Cys His Gln Ser Ile Leu Glu Leu Phe Asn Thr Ser Tyr Cys 325 330 335		
Pro Tyr Ser Gln Cys Ala Phe Asn Gly Ile Phe Leu Pro Pro Leu Gln 340 345 350		
Gly Asp Phe Gly Ala Phe Ser Ala Phe Tyr Phe Val Met Lys Phe Leu 355 360 365		
Asn Leu Thr Ser Glu Lys Val Ser Gln Glu Lys Val Thr Glu Met Met 370 375 380		
Lys Lys Phe Cys Ala Gln Pro Trp Glu Glu Ile Lys Thr Ser Tyr Ala 385 390 395 400		
Gly Val Lys Glu Lys Tyr Leu Ser Glu Tyr Cys Phe Ser Gly Thr Tyr 405 410 415		
Ile Leu Ser Leu Leu Leu Gln Gly Tyr His Phe Thr Ala Asp Ser Trp 420 425 430		
Glu His Ile His Phe Ile Gly Lys Ile Gln Gly Ser Asp Ala Gly Trp 435 440 445		
Thr Leu Gly Tyr Met Leu Asn Leu Thr Asn Met Ile Pro Ala Glu Gln 450 455 460		
Pro Leu Ser Thr Pro Leu Ser His Ser Thr 465 470		

<210> 29

<211> 473

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: Fusion  
construct of human CD39

<400> 29

Met Ala Leu Trp Ile Asp Arg Met Gln Leu Leu Ser Cys Ile Ala Leu  
1 5 10 15

Ser Leu Ala Leu Val Thr Asn Ser Ser Thr Lys Lys Thr Gln Leu Thr  
20 25 30

Ser Ser Thr Gln Asn Lys Ala Leu Pro Glu Asn Val Lys Tyr Gly Ile  
35 40 45

Val Leu Asp Ala Gly Ser Ser His Thr Ser Leu Tyr Ile Tyr Lys Trp  
50 55 60

Pro Ala Glu Lys Glu Asn Asp Thr Gly Val Val His Gln Val Glu Glu  
65 70 75 80

Cys Arg Val Lys Gly Pro Gly Ile Ser Lys Phe Val Gln Lys Val Asn  
85 90 95

Glu Ile Gly Ile Tyr Leu Thr Asp Cys Met Glu Arg Ala Arg Glu Val  
100 105 110

Ile Pro Arg Ser Gln His Gln Glu Thr Pro Val Tyr Leu Gly Ala Thr  
115 120 125

Ala Gly Met Arg Leu Leu Arg Met Glu Ser Glu Glu Leu Ala Asp Arg  
130 135 140

Val Leu Asp Val Val Glu Arg Ser Leu Ser Asn Tyr Pro Phe Asp Phe  
145 150 155 160

Gln Gly Ala Arg Ile Ile Thr Gly Gln Glu Glu Gly Ala Tyr Gly Trp  
165 170 175

Ile Thr Ile Asn Tyr Leu Leu Gly Lys Phe Ser Gln Lys Thr Arg Trp  
180 185 190

Phe Ser Ile Val Pro Tyr Glu Thr Asn Asn Gln Glu Thr Phe Gly Ala  
195 200 205

Leu Asp Leu Gly Gly Ala Ser Thr Gln Val Thr Phe Val Pro Gln Asn  
210 215 220

Gln Thr Ile Glu Ser Pro Asp Asn Ala Leu Gln Phe Arg Leu Tyr Gly  
225 230 235 240

Lys Asp Tyr Asn Val Tyr Thr His Ser Phe Leu Cys Tyr Gly Lys Asp  
245 250 255

Gln Ala Leu Trp Gln Lys Leu Ala Lys Asp Ile Gln Val Ala Ser Asn  
260 265 270

Glu Ile Leu Arg Asp Pro Cys Phe His Pro Gly Tyr Lys Lys Val Val  
275 280 285

Asn Val Ser Asp Leu Tyr Lys Thr Pro Cys Thr Lys Arg Phe Glu Met  
290 295 300

Thr Leu Pro Phe Gln Gln Phe Glu Ile Gln Gly Ile Gly Asn Tyr Gln







